WEST Search History

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DATE: Wednesday, July 28, 2004

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ		
☐	L6	L5 not l2	149
☐	L5	l4 and (e adj3 c 2.3.1.51 or lpaat or lysophosphatidic acid transferase)	159
☐	L4	L1 and (gene or nucleic acid or cdna or dna or mrna)	734
☐	L3	L1 and (gene or nucleic acid or cdna or dna or mrna)	734
☐	L2	(soybean or soy bean or glycine max) same (acyltransferase or e adj3 c 2.3.1.51 or lpaat or lysophosphatidic acid transferase)	33
☐	L1	(soybean or soy bean or glycine max) and (acyltransferase or e adj3 c 2.3.1.51 or lpaat or lysophosphatidic acid transferase)	762

END OF SEARCH HISTORY

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=> file .nash
=> s glycine max or soybean
L1         18386 FILE MEDLINE
L2        100963 FILE CAPLUS
L3         41041 FILE SCISEARCH
L4          9004 FILE LIFESCI
L5         65555 FILE BIOSIS
L6         13022 FILE EMBASE

TOTAL FOR ALL FILES
L7        247971 GLYCINE MAX OR SOYBEAN

=> s soy bean

TOTAL FOR ALL FILES
L14         7852 SOY BEAN

=> s l7 or l14
TOTAL FOR ALL FILES
L21       253447 L7 OR L14

=> s l21 and (acyltransferase or e(3w)c (1w)2.3.1.51 or lpaat or lysophosphatidic acid
transferase)
TOTAL FOR ALL FILES
L28          409 L21 AND (ACYLTRANSFERASE OR E(3W)C (1W)2.3.1.51 OR LPAAT OR
                 LYSOPHOSPHATIDIC ACID TRANSFERASE)

=> s l26 and (gene or cdna or nucleic acid or dna or mrna or clon?)
TOTAL FOR ALL FILES
L35           93 L26 AND (GENE OR CDNA OR NUCLEIC ACID OR DNA OR MRNA OR CLON?)

=> s l35 not 2001-2004/py
TOTAL FOR ALL FILES
L42           47 L35 NOT 2001-2004/PY

=> dup rem l42
PROCESSING COMPLETED FOR L42
L43           38 DUP REM L42 (9 DUPLICATES REMOVED)

=> d ibib abs 1-38

L43  ANSWER 1 OF 38  CAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2000:742235  CAPLUS
DOCUMENT NUMBER:          133:291952
TITLE:                    Modification of lipid biosynthesis by DNA
                          shuffling
INVENTOR(S):              Yuan, Ling; Raillard, Sun Ai; Lassner, Michael
PATENT ASSIGNEE(S):       Maxygen, Inc., USA
SOURCE:                   PCT Int. Appl., 90 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.          KIND  DATE           APPLICATION NO.   DATE
     ----------------    ----  --------       ----------------  --------
     WO 2000061740        A1   20001019       WO 2000-US9285    20000406
         W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,
             CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
             IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
             MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
             SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM,
             AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
             DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
             CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
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PRIORITY APPLN. INFO.: US 1999-128707P P 19990410

AB Methods of modulating lipid prodn. in cells and whole organisms by **DNA** shuffling are provided. Single **genes**, operons, lipid biosynthetic cycles and whole genomes can be recombined to produce cells and organisms with desirable lipid synthetic or metabolic activity. Libraries of recombined lipid synthetic **nucleic acids** and organisms are also provided. Modification of lipid satn., fatty acid compn., fatty alc. compn., wax compn., acyl chain length, location of fatty acid accumulation, triglyceride yield, substrate specificity, expression level, are described. A decrease in susceptibility to protease cleavage, high or low pH levels, extreme temps., are also claimed. A decrease in toxicity, and modification of methyltransferase activity resulting in formation of branched chain, cyclopropyl, methoxy, or keto fatty acids, are also described. Use of two-hybrid system in detecting the changes in lipid biosynthetic activity is also claimed. Screening of libraries, such as phage display library is described. Crop plants such as corn, peanut, barley, millet, rice, **soybean**, sorghum, wheat, oats, sunflower, or nut whose lipid biosynthetic activity modified, are claimed. **DNA** shuffling is a powerful process for directed evolution, which generates diversity by recombination, combining useful mutations from individual **genes**.

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L43 ANSWER 2 OF 38 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:384442 CAPLUS

DOCUMENT NUMBER: 133:27387

TITLE: Polynucleotides (**cDNA**) and polypeptides of plant lecithin cholesterol **acyltransferase** sequence homologs, sequences and biological uses thereof

INVENTOR(S): Cahoon, Rebecca E.; Kinney, Anthony J.; Sakai, Hajime; Shen, Jennie Bih-jien; Butler, Karlene H.; Saylor, James J.

PATENT ASSIGNEE(S): E. I. Du Pont de Nemours & Co., USA

SOURCE: PCT Int. Appl., 49 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000032791	A2	20000608	WO 1999-US28586	19991202
WO 2000032791	A3	20000914		

W: AE, AL, AU, BA, BB, BG, BR, CA, CN, CR, CU, CZ, DM, EE, GD, GE, HR, HU, ID, IL, IN, IS, JP, KP, KR, LC, LK, LR, LT, LV, MG, MK, MN, MX, NO, NZ, PL, RO, SG, SI, SK, SL, TR, TT, UA, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1998-110782P P 19981203

AB The invention provides **cDNA** mols. encoding corn and **soybean** lecithin:cholesterol **acyltransferases** (LCAT) based on sequence homol. to known LCATs. The invention also provides a chimeric **gene** comprising the plant LCAT **cDNA** operably linked to suitable regulatory sequences (such as promoter and terminator sequences) and a host cell (such as yeast, bacteria, plant or virus) transformed with said chimeric **gene** for the recombinant prodn. of the LCAT. The invention further provides for the use of: (1) plant LCAT-specific primers for amplification of a **nucleic acid** encoding LCAT; (2) plant LCAT-specific probes in screening a **cDNA** or genomic library for **nucleic acid** mols. encoding LCAT and (3) polynucleotides comprising at least 30 nucleotides of the LCAT **cDNA** mol. or complement of such sequence, used for identifying an polynucleotide that affects the level of LCAT expression. Finally, the invention provides: (1) a method for evaluating the ability of a mol. to inhibit the activity of LCAT and (2) a method for selecting transformed plant cells overexpressing LCAT, which involves measuring the

phytosterol concn. in the cell. **CDNA** and amino acid sequences of full length and partial **cDNA clones** encoding the corn LCAT sequence homologs are provided. Likewise, **cDNA** and amino acid sequences of a full length and a partial **cDNA clone** encoding **soybean** LCAT sequence homologs are provided. Using the BLASTX algorithm, the amino acid sequences of various putative corn LCATs were found to be 29.4% to 37.2% similar to the amino acid sequence of Arabidopsis thaliana GenBank accession no. AC004557 GI3935185, while the sequence of the putative **soybean** LCAT was found to be 57.% similar to the sequence of A. thaliana. The invention also discussed that overexpression or cosuppression of LCAT may be useful to genetically alter the content of phytosterol or lecithin in grains.

L43 ANSWER 3 OF 38 MEDLINE on STN
ACCESSION NUMBER: 1999277595 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10350092
TITLE: Enhanced expression and differential inducibility of **soybean** chalcone synthase **genes** by supplemental UV-B in dark-grown seedlings.
AUTHOR: Shimizu T; Akada S; Senda M; Ishikawa R; Harada T; Niizeki M; Dube S K
CORPORATE SOURCE: Plant Breeding Laboratory, Faculty of Agriculture, Hirosaki University, Japan.
SOURCE: Plant molecular biology, (1999 Mar) 39 (4) 785-95. Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990628
Last Updated on STN: 19990628
Entered Medline: 19990615

AB By developing **gene**-specific RT-PCR and using filters to allow transmission down to 290 nm (UV-B+) or blocking all radiation below 320 nm (UV-B(-)), the effect of UV-B+ and UV-B- light on expression of each of the presently known seven members of **soybean** chalcone synthase (CHS) **gene** family in dark-grown seedlings was analyzed. Dark expression was detectable already in 18 h dark-germinating embryos, with progressive increases on successive days, suggesting that chs belongs to a class of **genes** expressed very early during germination, and that the expression at this stage is either constitutive or induced by non-light-dependent factors present in the seed or made available following imbibition. Exposure of 18 h dark-germinating embryos to UV-B- or to UV-B+ light did not lead to an increase in chs signal. However, the 24 h dark-germinating embryos showed a distinct effect of UV-B+, interestingly coinciding with the stage when the head of seedlings was in the process of being pushed up above ground by stem elongation, suggesting the possibility of a developmental switch modulating the appearance of UV-B response. The response to UV-B- was most prominent in chs1 and almost silent in chs2, while the up-regulation by UV-B+ was most prominent in chs5 and chs6 and much less so in chs2. Interestingly, chs2 was noted to be the only member of the Gmchs **gene** family devoid of H-box, raising the possibility that the H-box may be a good indicator of the photo-inducibility of a chs **gene**.

L43 ANSWER 4 OF 38 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 1999:811077 SCISEARCH
THE GENUINE ARTICLE: 247FQ
TITLE: The Arabidopsis thaliana TAG1 mutant has a mutation in a diacylglycerol **acyltransferase gene**
AUTHOR: Zou J T; Wei Y D; Jako C; Kumar A; Selvaraj G; Taylor D C (Reprint)
CORPORATE SOURCE: NATL RES COUNCIL CANADA, INST PLANT BIOTECHNOL, 110 GYMNASIUM PL, SASKATOON, SK S7N 0W9, CANADA (Reprint); NATL RES COUNCIL CANADA, INST PLANT BIOTECHNOL, SASKATOON, SK S7N 0W9, CANADA
COUNTRY OF AUTHOR: CANADA
SOURCE: PLANT JOURNAL, (SEP 1999) Vol. 19, No. 6, pp. 645-653. Publisher: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 0NE, OXON, ENGLAND.

ISSN: 0960-7412.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI
LANGUAGE: English
REFERENCE COUNT: 35
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB In Arabidopsis thaliana (ecotype Columbia) mutant line AS11, an EMS-induced mutation at a locus on chromosome II results: in a reduced diacylglycerol **acyltransferase** (DGAT; EC 2.3.1.20) activity, reduced seed triacylglycerol, an altered seed fatty acid composition, and delayed seed development. A mutation has been identified in AS11 in a **gene**, which we designated as TAG?, that encodes a protein with an amino acid sequence which is similar to a recently reported mammalian DGAT, and, to a lesser extent, to acyl CoA:cholesterol **acyltransferases**. Molecular analysis revealed that the mutant allele in AS11 has a 147bp insertion located at the central region of intron 2. At the RNA level, an 81bp insertion composed entirely of an exon2 repeat was found in the transcript. While the seed triacylglycerol content is reduced by the lesion in AS11, there is no apparent effect on sterol ester content in the mutant seed. The TAG1 **cDNA** was over-expressed in yeast, and its activity as a microsomal DGAT confirmed. Therefore, the TAG? locus encodes a diacylglycerol **acyltransferase** , and the insertion mutation in the TAG1 **gene** in mutant AS11 results in its altered lipid phenotype.

L43 ANSWER 5 OF 38 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 1998:506998 CAPLUS
DOCUMENT NUMBER: 129:214116
TITLE: Relation between diacylglycerol **acyltransferase** activity and oil concentration in **soybean**
AUTHOR(S): Settlage, Sharon B.; Kwanyuen, Prachuab; Wilson, Richard F.
CORPORATE SOURCE: Department of Biochemistry, North Carolina State University, Raleigh, NC, 27695-7622, USA
SOURCE: Journal of the American Oil Chemists' Society (1998), 75(7), 775-781
CODEN: JAOCA7; ISSN: 0003-021X
PUBLISHER: AOCS Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Diacylglycerol **acyltransferase** (EC 2.3.1.20; DGAT) catalyzes synthesis of triacylglycerol from acyl-CoA and diacylglycerol. Activity of this enzyme and developmental changes in oil accumulation were estd. at various stages of seed growth in **soybean** germplasm with phenotypic differences in oil content. Oil deposition in seed of these genotypes followed a sigmoid pattern that was modeled to predict incremental rates of oil accumulation during seed development. A strong pos. correlation was found between the estd. peak rate of oil deposition (near the mid-term of seed development) and oil concn. in mature seed. At satg. substrate levels, DGAT activity measured near the peak rate of oil deposition also was correlated pos. with oil phenotype. In the latter stages of seed development, a pos. correlation between ests. of enzyme activity at or below the apparent Km for diolein and comparable oil accumulation rates was attributed to reduced synthesis of substrates and/or potential change in affinity for substrate as suggested by an increase in apparent Km for diolein in older seed. These data indicated that DGAT activity may be a rate-limiting step in triacylglycerol synthesis. However, it is difficult to accept the idea of a single rate-limiting step at the end of a complex metabolic pathway. Because oil is a quant. inherited trait, several **genes** det. genotypic differences in oil content among **soybeans**. Hence, DGAT activity may be an indicator of coordinated genetic expression of **gene** -products in the entire glycerolipid synthetic pathway for a given genotype. In any case, results of this investigation demonstrated that genotypic differences in DGAT activity contributed to expression of genetic variation in oil content among **soybean** germplasm.

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L43 ANSWER 6 OF 38 MEDLINE on STN

ACCESSION NUMBER: 97134967 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8980527
TITLE: Isolation of **cDNAs** encoding two purine biosynthetic enzymes of **soybean** and expression of the corresponding transcripts in roots and root nodules.
AUTHOR: Schnorr K M; Laloue M; Hirel B
CORPORATE SOURCE: Laboratoire de Biologie Cellulaire, INRA, Centre de Versailles, Versailles, France.
SOURCE: Plant molecular biology, (1996 Nov) 32 (4) 751-7.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 20000303
Entered Medline: 19970130

AB **Soybean** nodule **cDNA clones** encoding glycinamide ribonucleotide (GAR) synthetase (GMpurD) and GAR transformylase (GMpurN) were isolated by complementation of corresponding Escherichia coli mutants. GAR synthetase and GAR transformylase catalyse the second and the third steps in the de novo purine biosynthesis pathway, respectively. One class of GAR synthetase and three classes of GAR transformylase **cDNA clones** were identified. Northern blot analysis clearly shows that these purine biosynthetic **genes** are highly expressed in young and mature nodules but weakly expressed in roots and leaves. Expression levels of GMpurD and GMpurN **mRNAs** were not enhanced when ammonia was provided to non-nodulated roots.

L43 ANSWER 7 OF 38 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 1995:578993 CAPLUS
DOCUMENT NUMBER: 123:4178
TITLE: Purification and Reconstitution of Murine Mitochondrial Glycerol-3-phosphate **Acyltransferase**. Functional Expression in Baculovirus-Infected Insect Cells
AUTHOR(S): Yet, Shaw-Fang; Moon, Yangha Kim; Sul, Hei Sook
CORPORATE SOURCE: Department of Nutritional Sciences, University of California, Berkeley, CA, 94720, USA
SOURCE: Biochemistry (1995), 34(22), 7303-10
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Glycerol-3-phosphate **acyltransferase** (GPAT) catalyzes the initial step in glycerolipid biosynthesis. We recently **cloned** a **cDNA** to a 6.8-kb **mRNA**, a message that can be induced dramatically by feeding a high-carbohydrate diet [Paulauskis & Sul (1988) J. Biol. Chem. 263, 7049-7054; Shin et al. (1991) J. Biol. Chem. 266, 23834-23839], and identified the open reading frame, p90, as mitochondrial GPAT [Yet et al. (1993) Biochem. 32, 9486-9491]. To initiate characterization of mitochondrial GPAT, we purified and reconstituted the GPAT activity using phospholipids after expressing functional enzyme in Sf9 insect cells. Infection with recombinant virus contg. p90 sequence resulted in high levels of GPAT expression in mitochondria, compared to noninfected cellss or cells infected with the reverse orientation insertion baculovirus. There was a dramatic increase in N-ethylmaleimide-resistant mitochondrial GPAT activity. The GPAT protein was not detectable by Western blot in noninfected Sf9 cells or in cells infected with the GPAT sequence in the reverse orientation. However, in cells infected with GPAT in the correct orientation, there was a dramatic increase in the GPAT protein that was readily detectable by Coomassie staining both in total exts. and in the mitochondrial fraction. To ease the purifn., we next expressed GPAT as a polyhistidine fusion protein in insect cells. The polyhistidine tag did not interfere with targeting to mitochondria or with the catalytic activity of GPAT. After solubilization of the mitochondrial fraction with the nonionic detergent C12E8, we purified the GPAT fusion protein using a Ni2+ matrix column. The purified p90 protein was not enzymically active, but the GPAT activity could be reconstituted by adding crude **soybean** phosphatidylcholine.

Other phospholipids in decreasing order of effectiveness in reconstituting GPAT activity were phosphatidylserine, phosphatidylinositol, and phosphatidylethanolamine. Cardiolipin, a major mitochondrial membrane phospholipid, was least effective. Using GPAT expressed in mitochondria of the Sf9 insect cells, we detd. the apparent Km value for glycerol 3-phosphate to be 0.67 mM. When various fatty acyl-CoAs were compared as acyl donors, GPAT showed preference for satd. fatty acyl-CoAs from carbon lengths of 8 to 16 as substrate, and unsatd. fatty acyl-CoAs tested were only 20% as effective. We also demonstrated that the catalytic activity of GPAT was lost when a stretch of 78 amino acids (aa 250-327), a region that has sequence homol. to Escherichia coli GPAT, was deleted. GPAT, expressed at a high level in mitochondria employing a baculovirus system, can be purified in a single step and will be useful in the future for the structure-function studies.

L43 ANSWER 8 OF 38 MEDLINE on STN
ACCESSION NUMBER: 96046740 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7579172
TITLE: Organization of **soybean** chalcone synthase **gene** clusters and characterization of a new member of the family.
AUTHOR: Akada S; Dube S K
CORPORATE SOURCE: Center for Agricultural Biotechnology, University of Maryland, College Park 20742, USA.
SOURCE: Plant molecular biology, (1995 Oct) 29 (2) 189-99. Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L07647
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19960124
Entered Medline: 19951204

AB Chalcone synthase (CHS; EC 2.3.1.74), the first committed enzyme of the multibranched pathway of flavonoid/isoflavonoid biosynthesis is encoded by a multigene family in **soybean,** (**Glycine max** L. Merrill). Our results suggest that this **gene** family comprises at least seven members, some of which are clustered. We have identified four chs clusters in the allo-tetraploid G. max genome and chs5, a newly characterized member of the chs **gene** family is present in two of them. We describe the complete nucleotide sequence of chs5, the identification of its immediate neighbors and the organization of the four hitherto identified chs clusters in the Gm genome.

L43 ANSWER 9 OF 38 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:624996 CAPLUS
DOCUMENT NUMBER: 121:224996
TITLE: **DNA** encoding 2-**acyltransferases** and its use in altering the fatty acid profile of plant oils
INVENTOR(S): Slabas, Antoni Ryszard; Brown, Adrian Paul
PATENT ASSIGNEE(S): Nickerson Biocem Ltd., UK
SOURCE: PCT Int. Appl., 45 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9413814	A1	19940623	WO 1993-GB2528	19931210
W: AU, BB, BG, BR, BY, CA, CZ, FI, HU, JP, KP, KR, KZ, LK, LV, MG, MN, MW, NO, NZ, PL, RO, RU, SD, SK, UA, US, VN				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2151147	AA	19940623	CA 1993-2151147	19931210
AU 9456567	A1	19940704	AU 1994-56567	19931210
AU 694098	B2	19980716		

EP 673424	A1	19950927	EP 1994-902058	19931210	
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE					
HU 71785	A2	19960228	HU 1995-1694	19931210	
PL 176961	B1	19990831	PL 1993-309327	19931210	
US 5843739	A	19981201	US 1995-454267	19950804	
US 5945323	A	19990831	US 1997-941319	19970930	
AU 9889323	A1	19981203	AU 1998-89323	19981015	
PRIORITY APPLN. INFO.:			GB 1992-25845	A 19921210	
			AU 1994-56567	A3 19931210	
			WO 1993-GB2528	W 19931210	

AB The expression of foreign **genes** for insol. **acyltransferases**, esp. 2-**acyltransferases**, in transgenic plants is used to modify the fatty acid compn. of the glyceridic oils of the plant. For example, oil seed rape (Brassica napus) may contain a 2-**acyltransferase gene** derived from Limnanthes douglasii in order to increase the erucic acid content of the oil. Antisense expression constructs or ribozymes may also be used to limit expression of the endogenous **acyltransferase gene**. A **cDNA** sequence for maize (Zea mays) 2-**acyltransferase** is disclosed and is useful for **cloning acyltransferase genes** and/or **cDNAs** from other organisms, including L. douglasii.

L43 ANSWER 10 OF 38 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN

ACCESSION NUMBER:	94:514813 SCISEARCH
THE GENUINE ARTICLE:	PD075
TITLE:	NATURAL AUTOANTIBODY AGAINST APOLIPOPROTEIN A-I - DETECTION AND CHARACTERIZATION OF THE MONOCLONAL-ANTIBODY ESTABLISHED FROM NORMAL UNIMMUNIZED BALB/C MICE
AUTHOR:	IMAI H; SUZUKI S; UCHIDA K; KIKUCHI K; SUGIYAMA H; KOHNO H; UMEDA M (Reprint); INOUE K
CORPORATE SOURCE:	TOKYO METROPOLITAN INST MED SCI, DEPT INFLAMMAT RES, BUNKYO KU, 18-22 HONKOMAGONE 3 CHOME, TOKYO 113, JAPAN (Reprint); UNIV TOKYO, FAC PHARMACEUT SCI, DEPT HLTH CHEM, TOKYO 113, JAPAN; ASAHI DENKA KOGYO KK, TOKYO, JAPAN
COUNTRY OF AUTHOR:	JAPAN
SOURCE:	JOURNAL OF IMMUNOLOGY, (01 SEP 1994) Vol. 153, No. 5, pp. 2290-2301. ISSN: 0022-1767.
DOCUMENT TYPE:	Article; Journal
FILE SEGMENT:	LIFE
LANGUAGE:	ENGLISH
REFERENCE COUNT:	51

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB During the course of studying the immunogenicity of **soybean** lipids, we observed frequent production of the mAbs that bind to apolipoprotein A-I (apoA-I) when spleen cells from unimmunized normal BALB/c mice were employed for fusion. Of the 986 colonies from six fusions, 38 (3.9% of the total) were directed against apoA-I and 13 mAbs (IgM) were established for further analysis. The following lines of evidence indicate that this family of mAb may form a novel family of natural autoantibodies against apoA-I: 1) The mAbs were shown to bind effectively to high density lipoprotein from various species, including BALB/c mouse, and immunoblotting analyses revealed that the mAbs bound specifically to the 28-kDa protein of high density lipoprotein. 2) The 28-kDa protein was purified to homogeneity and identified as apoA-I by amino acid sequence analyses and by its cross-reactivity with a xenogenic anti-apoA-I mAb (**clone** A/11). 3) Differing from the xenogenic anti-apoA-I mAb, the present mAb did not bind to native apoA-I, whereas an effective binding was observed only when the apoA-I had formed a complex with neutral lipids containing polyunsaturated fatty acids such as trilinoleoylglycerol and 5-cholesten-3 beta-ol 3-linoleate. 4) Sera from unimmunized BALB/c mice had readily detectable Abs against apoA-I and the majority of the serum autoantibodies were of the IgA and IgM isotype. 5) The anti-apoA-I mAbs displayed a functional heterogeneity in their reactivity with polyanionic substances and some of the mAbs established showed an extensive cross-reaction with polyanionic substances such as ssDNA and cardiolipin.

L43 ANSWER 11 OF 38 MEDLINE on STN DUPLICATE 3

ACCESSION NUMBER:	95054523 MEDLINE
DOCUMENT NUMBER:	PubMed ID: 7965198

TITLE: Dietary fat saturation affects apolipoprotein **gene** expression and high density lipoprotein size distribution in golden Syrian hamsters.
AUTHOR: Ahn Y S; Smith D; Osada J; Li Z; Schaefer E J; Ordovas J M
CORPORATE SOURCE: Lipid Metabolism Laboratory, USDA Human Nutrition Research Center on Aging, Tufts University, Boston, MA 02111.
CONTRACT NUMBER: HL39326 (NHLBI)
SOURCE: Journal of nutrition, (1994 Nov) 124 (11) 2147-55.
Journal code: 0404243. ISSN: 0022-3166.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199412
ENTRY DATE: Entered STN: 19950110
Last Updated on STN: 19950110
Entered Medline: 19941216

AB Our purpose was to elucidate the mechanisms whereby diets high in polyunsaturated fat lower plasma triglycerides and HDL cholesterol concentrations compared with diets high in saturated fat. Twenty-four male Golden Syrian hamsters (F1B strain) were fed semipurified diets containing 0.2 g cholesterol + 15 g fat/100 g diet enriched (13 g/100 g) in either coconut oil or **soybean** oil for 18 wk. Consumption of the **soybean** oil diet was associated with significantly ($P < 0.001$) lower mean concentrations of HDL cholesterol (28%), triglycerides (51%) and free fatty acids (51%), as well as a significantly lower proportion of large HDL particles. No effect on plasma cholesteryl ester transfer protein or lecithin:cholesterol **acyltransferase** activities or hepatic or intestinal apolipoprotein (apo) A-I, A-IV or E **mRNA** levels were noted. The **soybean** oil-fed group had significantly lower levels of **mRNA** ($P < 0.05$) for hepatic apo A-II (23%) and apo C-III (18%) and significantly higher levels of **mRNA** for intestinal apo C-II (23%). Our data are consistent with the hypothesis that diets high in polyunsaturated fatty acids lower triglyceride concentrations in hamsters by decreasing apo C-III **gene** expression and by increasing apo C-II **gene** expression. In addition, reduced expression of apo A-II in animals fed the **soybean** oil diet may contribute to the lower HDL cholesterol concentration and larger proportion of small HDL particles noted.

L43 ANSWER 12 OF 38 MEDLINE on STN
ACCESSION NUMBER: 94345010 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8066134
TITLE: Chalcone synthase **mRNA** and activity are reduced in yellow **soybean** seed coats with dominant I alleles.
AUTHOR: Wang C S; Todd J J; Vodkin L O
CORPORATE SOURCE: Department of Agronomy, University of Illinois, Urbana 61801.
SOURCE: Plant physiology, (1994 Jun) 105 (2) 739-48.
Journal code: 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19941005
Last Updated on STN: 19941005
Entered Medline: 19940920

AB The seed of all wild Glycine accessions have black or brown pigments because of the homozygous recessive i allele in combination with alleles at the R and T loci. In contrast, nearly all commercial **soybean** (**Glycine max**) varieties are yellow due to the presence of a dominant allele of the I locus (either I or i) that inhibits pigmentation in the seed coats. Spontaneous mutations to the recessive i allele occur in these varieties and result in pigmented seed coats. We have isolated a **clone** for a **soybean** dihydroflavonol reductase (DFR) **gene** using polymerase chain reaction. We examined expression of DFR and two other **genes** of the flavonoid pathway during **soybean** seed coat development in a series of near-isogenic isolines that vary in pigmentation as specified by

combinations of alleles of the I, R, and T loci. The expression of phenylalanine ammonia-lyase and DFR **mRNAs** was similar in all of the **gene** combinations at each stage of seed coat development. In contrast, chalcone synthase (CHS) **mRNA** was barely detectable at all stages of development in seed coats that carry the dominant I allele that results in yellow seed coats. CHS activity in yellow seed coats (I) was also 7- to 10-fold less than in the pigmented seed coats that have the homozygous recessive i allele. It appears that the dominant I allele results in reduction of CHS **mRNA**, leading to reduction of CHS activity as the basis for inhibition of anthocyanin and proanthocyanin synthesis in **soybean** seed coats. A further connection between CHS and the I locus is indicated by the occurrence of multiple restriction site polymorphisms in genomic **DNA** blots of the CHS **gene** family in near-isogenic lines containing alleles of the I locus.

L43 ANSWER 13 OF 38 MEDLINE on STN
ACCESSION NUMBER: 94355680 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8075422
TITLE: Rhizobium inoculation and physical wounding result in the rapid induction of the same chalcone synthase copy in Trifolium subterraneum.
AUTHOR: Lawson C G; Djordjevic M A; Weinman J J; Rolfe B G
CORPORATE SOURCE: Center for Genetic Research (Plant Microbe Interactions Group), Research School of Biological Sciences, Australian National University, Canberra City.
SOURCE: Molecular plant-microbe interactions : MPMI, (1994 Jul-Aug) 7 (4) 498-507.
Journal code: 9107902. ISSN: 0894-0282.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19941013
Last Updated on STN: 19941013
Entered Medline: 19940930

AB The **gene** or **genes** encoding chalcone synthase (CHS) in the legume Trifolium subterraneum (subterranean clover) were induced within 6 hr after inoculation with Rhizobium leguminosarum bv. trifolii strain ANU843. No induction was found in uninoculated controls or plants inoculated with either the nodulation-deficient R. l. bv. trifolii strain ANU845 (pSym-) or R. meliloti strain 1021, which is capable of nodulating alfalfa but not clover. Morphological examination of the interaction between the legume and bacteria in this system showed that root hair distortion (a marker of the early events in the interaction) was apparent within 10 hr after inoculation. This indicated that CHS induction could occur before any detectable sign of rhizobial penetration of root hairs. The addition of a crude preparation of R. l. bv. trifolii lipooligosaccharide signals (Nod metabolites) to the plant growth medium had no effect on the expression of CHS over 36 hr, although root hair distortion was apparent over this time. These treatments were then contrasted with physical wounding. Wounding the plants led to a rapid induction of CHS, occurring within 2 hr. Sequence analysis of **cloned** CHS **cDNA** from pools sampled after Rhizobium inoculation or wounding treatments showed the **gene** designated CHS5 was the major CHS species in both treatments. Conserved sequences were found in promoters of CHS5 and **soybean** Gmchs7, a **gene** which has overlapping expression patterns. These findings support the view that the induction of the phenylpropanoid pathway is involved in the very early events of the Rhizobium infection of legumes.

L43 ANSWER 14 OF 38 MEDLINE on STN
ACCESSION NUMBER: 95075295 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7984092
TITLE: Nod factors of Rhizobium are a key to the legume door.
AUTHOR: Relic B; Perret X; Estrada-Garcia M T; Kopcinska J; Golinowski W; Krishnan H B; Pueppke S G; Broughton W J
CORPORATE SOURCE: LBMPS, Universite de Geneve, Switzerland.
SOURCE: Molecular microbiology, (1994 Jul) 13 (1) 171-8.
Journal code: 8712028. ISSN: 0950-382X.

PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J03702; GENBANK-X73362
ENTRY MONTH: 199412
ENTRY DATE: Entered STN: 19950116
Last Updated on STN: 19960129
Entered Medline: 19941230

AB Symbiotic interactions between rhizobia and legumes are largely controlled by reciprocal signal exchange. Legume roots excrete flavonoids which induce rhizobial nodulation **genes** to synthesize and excrete lipo-oligosaccharide Nod factors. In turn, Nod factors provoke deformation of the root hairs and nodule primordium formation. Normally, rhizobia enter roots through infection threads in markedly curled root hairs. If Nod factors are responsible for symbiosis-specific root hair deformation, they could also be the signal for entry of rhizobia into legume roots. We tested this hypothesis by adding, at inoculation, NodNGR-factors to signal-production-deficient mutants of the broad-host-range Rhizobium sp. NGR234 and Bradyrhizobium japonicum strain USDA110. Between 10(-7) M and 10(-6) M NodNGR factors permitted these NodABC- mutants to penetrate, nodulate and fix nitrogen on Vigna unguiculata and **Glycine max**, respectively. NodNGR factors also allowed Rhizobium fredii strain USDA257 to enter and fix nitrogen on Calopogonium caeruleum, a nonhost. Detailed cytological investigations of V. unguiculata showed that the NodABC- mutant NGR delta nodABC, in the presence of NodNGR factors, entered roots in the same way as the wild-type bacterium. Since infection threads were also present in the resulting nodules, we conclude that Nod factors are the signals that permit rhizobia to penetrate legume roots via infection threads.

L43 ANSWER 15 OF 38 MEDLINE on STN
ACCESSION NUMBER: 94151453 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8108524
TITLE: Nucleotide sequence of a **soybean** chalcone synthase **gene** with a possible role in ultraviolet-B sensitivity, Gmchs6.
AUTHOR: Akada S; Kung S D; Dube S K
CORPORATE SOURCE: Center for Agricultural Biotechnology, University of Maryland, College Park 20742.
SOURCE: Plant physiology, (1993 Jun) 102 (2) 699-701.
Journal code: 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
OTHER SOURCE: GENBANK-L03352
ENTRY MONTH: 199403
ENTRY DATE: Entered STN: 19940330
Last Updated on STN: 19940330
Entered Medline: 19940323

L43 ANSWER 16 OF 38 MEDLINE on STN
ACCESSION NUMBER: 93250436 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8485404
TITLE: Dissection of the functional architecture of a plant defense **gene** promoter using a homologous in vitro transcription initiation system.
AUTHOR: Arias J A; Dixon R A; Lamb C J
CORPORATE SOURCE: Plant Biology Laboratory, Salk Institute for Biological Studies, La Jolla, California 92037.
SOURCE: Plant cell, (1993 Apr) 5 (4) 485-96.
Journal code: 9208688. ISSN: 1040-4651.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199306
ENTRY DATE: Entered STN: 19930618
Last Updated on STN: 19970203
Entered Medline: 19930608

AB CHS15 is one of a family of bean **genes** encoding chalcone synthase, which catalyzes the first reaction in a branch pathway of phenylpropanoid biosynthesis for the production of flavonoid pigments and UV protectants and isoflavonoid-derived phytoalexins. The functional architecture of the CHS15 promoter was dissected by a novel homologous plant in vitro transcription initiation system in which whole-cell and nuclear extracts from suspension-cultured **soybean** cells direct accurate and efficient RNA polymerase II-mediated transcription from an immobilized promoter template. Authentic transcription from the CHS15 promoter template was also observed with whole-cell extracts from suspension-cultured cells of bean, tobacco, and the monocot rice, and the **soybean** whole-cell extract transcribed several other immobilized promoter templates. Hence, this procedure may be of general use in the study of plant **gene** regulation mechanisms in vitro. Assay of the effects of depletion of the **soybean** whole-cell extract by preincubation with small regions of the CHS15 promoter or defined cis elements showed that trans factors that bind to G-box (CACGTG, -74 to -69) and H-box (CCTACC, -61 to -56 and -121 to -126) cis elements, respectively, make major contributions to the transcription of the CHS15 promoter in vitro. Both cis element/trans factor interactions in combination are required for maximal activity. Delineation of these functional cis element/trans factor interactions in vitro provides the basis for study of the mechanisms underlying developmental expression of CHS15 in pigmented petal cells established by G-box and H-box combinatorial interactions, and for characterization of the terminal steps of the signal pathway for stress induction of the phytoalexin defense response.

L43 ANSWER 17 OF 38 MEDLINE on STN
ACCESSION NUMBER: 94151429 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8108501
TITLE: Nucleotide sequence and putative regulatory elements of a nodule-development-specific member of the **soybean** (**Glycine max**) chalcone synthase multigene family, Gmchs 7.
AUTHOR: Akada S; Kung S D; Dube S K
CORPORATE SOURCE: Center for Agricultural Biotechnology, University of Maryland, College Park 20742.
SOURCE: Plant physiology, (1993 May) 102 (1) 321-3.
Journal code: 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M98871
ENTRY MONTH: 199403
ENTRY DATE: Entered STN: 19940330
Last Updated on STN: 19970203
Entered Medline: 19940323

L43 ANSWER 18 OF 38 MEDLINE on STN
ACCESSION NUMBER: 94151428 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8108500
TITLE: Nucleotide sequence and putative regulatory elements of **gene** 2 of the **soybean** (**Glycine max**) chalcone synthase multigene family.
AUTHOR: Akada S; Kung S D; Dube S K
CORPORATE SOURCE: Center for Agricultural Biotechnology, University of Maryland, College Park 20742.
SOURCE: Plant physiology, (1993 May) 102 (1) 317-9.
Journal code: 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X65636
ENTRY MONTH: 199403
ENTRY DATE: Entered STN: 19940330
Last Updated on STN: 19970203
Entered Medline: 19940323

L43 ANSWER 19 OF 38 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1993:402595 BIOSIS
DOCUMENT NUMBER: PREV199345061420
TITLE: Structural comparison between diacylglycerol **acyltransferase** and oil body associated protein.
AUTHOR(S): Kwanyuen, Prachuab [Reprint author]; Wilson, Richard F. [Reprint author]; Dewey, Ralph E.; Settlage, Sharon B.
CORPORATE SOURCE: United States Dep. Agric., Agric. Res. Serv., NC State Univ., Raleigh, NC 27695, USA
SOURCE: Plant Physiology (Rockville), (1993) Vol. 102, No. 1 SUPPL., pp. 72.
Meeting Info.: Joint Annual Meeting of the American Society of Plant Physiologists and the Canadian Society of Plant Physiologists (La Societe Canadienne de Physiologie Vegetale). Minneapolis, Minnesota, USA. July 31-August 4, 1993.
CODEN: PLPHAY. ISSN: 0032-0889.
DOCUMENT TYPE: Conference; (Meeting)
LANGUAGE: English
ENTRY DATE: Entered STN: 30 Aug 1993
Last Updated on STN: 31 Aug 1993

L43 ANSWER 20 OF 38 MEDLINE on STN
ACCESSION NUMBER: 92279242 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1594598
TITLE: Jasmonic acid/methyl jasmonate accumulate in wounded **soybean** hypocotyls and modulate wound **gene** expression.
AUTHOR: Creelman R A; Tierney M L; Mullet J E
CORPORATE SOURCE: Biotechnology Center, Ohio State University, Columbus 43210.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1992 Jun 1) 89 (11) 4938-41.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 199206
ENTRY DATE: Entered STN: 19920710
Last Updated on STN: 19920710
Entered Medline: 19920626
AB Jasmonic acid (JA) and its methyl ester, methyl jasmonate (MeJA), are plant lipid derivatives that resemble mammalian eicosanoids in structure and biosynthesis. These compounds are proposed to play a role in plant wound and pathogen responses. Here we report the quantitative determination of JA/MeJA in planta by a procedure based on the use of [13C,2H3]MeJA as an internal standard. Wounded **soybean** (**Glycine max** [L] Merr. cv. Williams) stems rapidly accumulated MeJA and JA. Addition of MeJA to **soybean** suspension cultures also increased **mRNA** levels for three wound-responsive **genes** (chalcone synthase, vegetative storage protein, and proline-rich cell wall protein) suggesting a role for MeJA/JA in the mediation of several changes in **gene** expression associated with the plants' response to wounding.

L43 ANSWER 21 OF 38 MEDLINE on STN
ACCESSION NUMBER: 94019265 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1339958
TITLE: [Molecular characteristics of chalcone synthase **gene** families from two cotton species using the polymerase chain reaction].
Molekuliarnaia kharakteristika semeistva genov khalkonsintazy dvukh vidov khlopchatnika s pomoshch'iu metoda polimeraznoi tsepnoi reaktsii.
AUTHOR: Byzova M V; Kraev A S; Pozmogova G E; Skriabin K G
SOURCE: Molekuliarnaia biologiia, (1992 Mar-Apr) 26 (2) 432-40.
Journal code: 0105454. ISSN: 0026-8984.
PUB. COUNTRY: RUSSIA: Russian Federation
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Russian

FILE SEGMENT: Priority Journals
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19940117
Entered Medline: 19931103

AB Using partial sequence data from a genomic **clone** and the fact of evolutionary conservation of chalcone synthase **genes**, two primers, corresponding to C-terminal peptides GGAACTCCCTTTTCTGGATAGCTCACC and CCTGGTCCGAACCCAAACAGGACGCCCC, were used to amplify, via polymerase chain reaction, genomic sequences from two Gossypium species, a diploid Gossypium herbaceum, and a tetraploid Gossypium hirsutum cv. 108F. Amplified **DNA** was separated into individual sequences by **cloning** into an M13 vector. Six different sequences were identified in each species. From each set of six, one sequence was found to be identical to the genomic sequence, which we have isolated from a subgenomic library of 108F **DNA** in lambda NM1149. Comparison of other sequences has allowed to find another pair of identical sequences, as well as to get an evidence, that the set isolated from the tetraploid cotton contained preferentially members of only one of the two subfamilies, probably due to primer specificity in amplification reaction. Comparison of specific amino acid substitutions in homologous sequences of cotton, peanut and **soybean** also suggested that all of the sequences isolated from cotton are more likely to code for chalcone synthase, that for a similar enzyme resveratrol synthetase.

L43 ANSWER 22 OF 38 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1992:466688 CAPLUS
DOCUMENT NUMBER: 117:66688
TITLE: Role of diacylglycerol **acyltransferase** in regulating oil content and composition in **soybean**
AUTHOR(S): Kwanyuen, Prachuab; Wilson, Richard F.
CORPORATE SOURCE: U. S. Dep. Agric., Raleigh, NC, 27695-7620, USA
SOURCE: Biotechnol. Nutr., Proc. Int. Symp., 3rd (1992), Meeting Date 1990, 413-33. Editor(s): Bills, Donald Duane; Kung, Shain-dow. Butterworth-Heinemann: Boston, Mass.
CODEN: 57TQAJ
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A review is given of factors affecting oil formation in **soybean** (**Glycine max**). Accessions of the USDA **Soybean** Germplasm Collection exhibit genetic diversity for oil concn. ranging from 12 to 27 percent of dry wt. Although oil concn. is a highly heritable quant. genetic trait, the genetic and biochem. basis for genotypic differences in the oil content of **soybean** seed is unknown. Information on biol. regulation of this trait has emerged from research on diacylglycerol **acyltransferase** (EC 2.3.1.20), the enzyme that catalyzes triacylglycerol synthesis. Diacylglycerol **acyltransferase** purified from the cv. Dare has a native mass of about 1.5 MDa. Structural anal. suggests the protein consists of 10 monomers having three nonidentical subunits in a 1:2:2 molar ratio. Kinetics of the enzyme purified from **soybeans** exhibiting high or low oil content suggest that genotypic differences in oil content may be governed by **gene** dosage effects. However, subtle conformational changes in protein structure may influence oil compn., as evidenced by apparent substrate specificities obsd. in germ-plasm contg. low-palmitic acid. Therefore, diacylglycerol **acyltransferase** may play a unique role in detg. the content and compn. of triacylglycerol in **soybean**.

L43 ANSWER 23 OF 38 MEDLINE on STN
ACCESSION NUMBER: 92161821 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1536573
TITLE: Expression **cloning** in Escherichia coli and preparative isolation of the reductase coacting with chalcone synthase during the key step in the biosynthesis of **soybean** phytoalexins.
AUTHOR: Welle R; Schroder J
CORPORATE SOURCE: Lehrstuhl fur Biochemie der Pflanzen, Biologisches Institut II, Universitat Freiburg, Germany.

SOURCE: Archives of biochemistry and biophysics, (1992 Mar) 293 (2) 377-81.
Journal code: 0372430. ISSN: 0003-9861.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199203
ENTRY DATE: Entered STN: 19920410
Last Updated on STN: 19920410
Entered Medline: 19920324

AB The **cDNA** for the reductase involved in the biosynthesis of 6'-deoxychalcone (4,2',4'-trihydroxychalcone), the first specific intermediate in the pathway to **soybean** phytoalexins, was **cloned** into the expression vector pKK233-2 and transformed into Escherichia coli. Using this source, about 5 mg of homogeneous reductase was isolated from 45 g of cells. The protein purification protocol differs completely from the scheme applied to **soybean** cell cultures. Size, N-terminal and specific enzyme activities were identical for the plant and E. coli protein. The pure protein is fairly stable, retaining 70% of initial activity after storage at 5 degrees C during 4 weeks. This protein is used for crystallization and in the study of its protein-protein interaction with chalcone synthase.

L43 ANSWER 24 OF 38 MEDLINE on STN
ACCESSION NUMBER: 91172838 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2006188
TITLE: Characterization of a nuclear protein that binds to three elements within the silencer region of a bean chalcone synthase **gene** promoter.
AUTHOR: Harrison M J; Lawton M A; Lamb C J; Dixon R A
CORPORATE SOURCE: Plant Biology Division, Samuel Roberts Noble Foundation, Ardmore, OK 73402.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1991 Mar 15) 88 (6) 2515-9.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199104
ENTRY DATE: Entered STN: 19910512
Last Updated on STN: 19910512
Entered Medline: 19910425

AB The chalcone synthase (EC 2.3.1.74) **gene** promoter from the bean Phaseolus vulgaris L. contains a silencer element between positions -140 and -326 fro the transcription start site that is functional in electroporated **soybean** protoplasts. This element contains three binding sites for a bean nuclear factor (SBF-1) with **DNA** sequence recognition properties that are very similar to those of nuclear factor GT-1. By using a synthetic tetramer of one of the binding sites as probe, we have purified sequence-specific SBF-1 activity approximately 1750-fold from suspension-cell nuclei, by using a combination of ammonium sulfate precipitation, gel filtration, heparin-agarose chromatography, and sequence-specific **DNA** affinity chromatography. The factor exhibited an apparent molecular weight of 160,000-200,000 on the basis of gel filtration. A subunit molecular weight of approximately 95,000 was determined from SDS/polyacrylamide gel electrophoretic analysis of purified fractions, followed by Southwestern blot analysis (a protein blot probed with oligonucleotide probes), and from UV-cross-linking experiments. The factor lost **DNA**-binding activity on treatment with alkaline phosphatase. We discuss the properties of SBF-1 in relation to the functionality of GT-1 binding sequences in plant **genes**.

L43 ANSWER 25 OF 38 MEDLINE on STN
ACCESSION NUMBER: 91329712 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1868209
TITLE: The nucleotide sequence of **gene** 1 of the **soybean** chalcone synthase multigene family.
AUTHOR: Akada S; Kung S D; Dube S K
CORPORATE SOURCE: Center for Agricultural Biotechnology, University of

Maryland, College Park 20742.
SOURCE: Plant molecular biology, (1991 Apr) 16 (4) 751-2.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X54644; GENBANK-X56749
ENTRY MONTH: 199109
ENTRY DATE: Entered STN: 19911006
Last Updated on STN: 19970203
Entered Medline: 19910913

L43 ANSWER 26 OF 38 MEDLINE on STN
ACCESSION NUMBER: 92003675 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1912487
TITLE: Water deficit modulates **gene** expression in growing zones of **soybean** seedlings. Analysis of differentially expressed **cDNAs**, a new beta-tubulin **gene**, and expression of **genes** encoding cell wall proteins.
AUTHOR: Creelman R A; Mullet J E
CORPORATE SOURCE: Department of Biochemistry and Biophysics, Texas A&M University, College Station 77843.
SOURCE: Plant molecular biology, (1991 Oct) 17 (4) 591-608.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
OTHER SOURCE: GENBANK-S54103; GENBANK-S59489; GENBANK-X55297; GENBANK-X55687; GENBANK-X55688; GENBANK-X55689; GENBANK-X55690; GENBANK-X56856; GENBANK-X58180; GENBANK-X59015; GENBANK-X60216
ENTRY MONTH: 199111
ENTRY DATE: Entered STN: 19920124
Last Updated on STN: 19970203
Entered Medline: 19911121

AB Transfer of **soybean** seedlings to low-water-potential vermiculite (psi w = -0.3 MPa) results in a reversible decrease in hypocotyl growth and modulation of several polysomal **mRNAs** (Plant Physiol 92: 205-214). We report here the isolation of two **cDNA clones** (pGE16 and pGE95) which correspond to **genes** whose **mRNA** levels are increased, and one **cDNA clone** (pGE23) which corresponds to a **gene** whose **mRNA** level is decreased in the hypocotyl zone of cell elongation by water deficit. In well-watered seedlings **mRNAs** hybridizing to pGE16 and pGE95 are most abundant in mature regions of the seedling, but in water-deficient seedlings **mRNA** levels are reduced in mature regions and enhanced in elongating regions. RNA corresponding to **soybean** proline-rich protein 1 (sbPRP1) shows a similar tissue distribution and response to water deficit. In contrast, in well-watered seedlings, the **gene** corresponding to pGE23 was highly expressed in the hypocotyl and root growing zones. Transfer of seedlings to low-water-potential vermiculite caused a rapid decrease in **mRNA** hybridizing to pGE23. Sequence analysis revealed that pGE23 has high homology with beta-tubulin. Water deficit also reduced the level of **mRNA** hybridizing to JCW1, an auxin-modulated **gene**, although with different kinetics. Furthermore, **mRNA** encoding actin, glycine-rich proteins (GRPs), and hydroxyproline-rich glycoproteins (HRGPs) were down-regulated in the hypocotyl zone of elongation of seedlings exposed to water deficit. No effect of water deficit was observed on the expression of chalcone synthase. Decreased expression of beta-tubulin, actin, JCW1, HRGP and GRP and increased expression of sbPRP1, pGE95 and pGE16 in the hypocotyl zone of cell elongation could participate in the reversible growth inhibition observed in water-deficient **soybean** seedlings.

L43 ANSWER 27 OF 38 MEDLINE on STN
ACCESSION NUMBER: 92190633 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1799701

TITLE: Sequence and analysis of the nodABC region of Rhizobium fredii USDA257, a nitrogen-fixing symbiont of **soybean** and other legumes.
AUTHOR: Krishnan H B; Pueppke S G
CORPORATE SOURCE: Department of Plant Pathology, University of Missouri, Columbia 65211.
SOURCE: Molecular plant-microbe interactions : MPMI, (1991 Sep-Oct) 4 (5) 512-20.
Journal code: 9107902. ISSN: 0894-0282.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J03702
ENTRY MONTH: 199204
ENTRY DATE: Entered STN: 19920509
Last Updated on STN: 19960129
Entered Medline: 19920421

AB We **cloned** and analyzed nodABC from Rhizobium fredii USDA257. These **genes** are thought to have common functions in initiation of nitrogen-fixing nodules by all rhizobia. In USDA257, they were located in a 9.2-kb EcoRI fragment that was not closely linked to either of two copies of the regulatory **gene**, nodD. nodABC was present in a 3,094-base pair (bp) sequenced region, which also included a consensus nod-box promoter. The three open reading frames contained 654, 642, and 1,239 bp, respectively, and encoded deduced proteins of 21.9, 23.4, and 44.7 kD. The sequence of the nodABC region of USDA257 was generally homologous with corresponding regions from other rhizobia, but it diverged significantly in the 5' non-translated region and in the 3'terminus of nodC. nodC was not translationally coupled to nodSU, as in another **soybean** symbiont, Bradyrhizobium japonicum, and the deduced NodC protein was the shortest of any such proteins yet described. Site-directed mutagenesis of the 9.2-kb EcoRI fragment confirmed that nodA, nodB, and nodC are essential for nodulation of **soybean**, but failed to identify other linked nod **genes**. Daidzein, a major isoflavone from **soybean** roots, was the most potent of nine tested flavonoids in activating a plasmid-borne nodC::lacZ fusion. The 9.2-kb fragment complemented nodA-, nodB-, and nodC- mutants of R. meliloti to the Nod+ phenotype on Medicago sativa, M. truncatula, and Trigonella foenum-graecum. Nodule numbers, percentage of nodulated plants, and shoot dry weights, however, were considerably less than in plants inoculated with mutants complemented with nodABC from R. meliloti.

L43 ANSWER 28 OF 38 MEDLINE on STN
ACCESSION NUMBER: 91177016 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1840523
TITLE: Induced plant responses to pathogen attack. Analysis and heterologous expression of the key enzyme in the biosynthesis of phytoalexins in **soybean** (**Glycine max** L. Merr. cv. Harosoy 63).
AUTHOR: Welle R; Schroder G; Schiltz E; Grisebach H; Schroder J
CORPORATE SOURCE: Institut fur Biologie II, Biochemie der Pflanzen, Universitat Freiburg, Federal Republic of Germany.
SOURCE: European journal of biochemistry / FEBS, (1991 Mar 14) 196 (2) 423-30.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M60269; GENBANK-M60270; GENBANK-M60271; GENBANK-M60272; GENBANK-M60273; GENBANK-M60352; GENBANK-M60353; GENBANK-M60354; GENBANK-X55730; GENBANK-X56530
ENTRY MONTH: 199104
ENTRY DATE: Entered STN: 19910519
Last Updated on STN: 19910519
Entered Medline: 19910426

AB In **soybean** (**Glycine max** L.), pathogen attack induces the formation of glyceollin-type phytoalexins. The biosynthetic key enzyme is a reductase which synthesizes 4,2', 4'-trihydroxychalcone in

co-action with chalcone synthase. Screening of a **soybean** **cDNA** library from elicitor-induced RNA in lambda gt11 yielded two classes of reductase-specific **clones**. The deduced proteins match to 100% and 95%, respectively, with 229 amino acids sequenced in the purified plant protein. Four **clones** of class A were expressed in Escherichia coli, and the proteins were tested for enzyme activity in extracts supplemented with chalcone synthase. All were active in 4,2',4'-trihydroxychalcone formation, and the quantification showed that shorter lengths of the **cDNAs** at the 5' end correlated with progressively decreasing enzyme activities. Genomic blots with **DNA** from plants capable of 4,2',4'-trihydroxychalcone synthesis revealed related sequences in bean (Phaseolus vulgaris L.) and peanut (Arachis hypogaea L.), but not in pea (Pisum sativum L.). No hybridization was observed with parsley (Petroselinum crispum) and carrot (Daucus carota) which synthesize other phytoalexins. The reductase protein contains a leucine-zipper motif and reveals a marked similarity with other oxidoreductases most of which are involved in carbohydrate metabolism.

L43 ANSWER 29 OF 38 MEDLINE on STN
ACCESSION NUMBER: 93005700 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1840912
TITLE: Differential expression of phenylalanine ammonia-lyase and chalcone synthase during **soybean** nodule development.
AUTHOR: Estabrook E M; Sengupta-Gopalan C
CORPORATE SOURCE: Department of Agronomy, New Mexico State University, Las Cruces 88003.
SOURCE: Plant cell, (1991 Mar) 3 (3) 299-308.
Journal code: 9208688. ISSN: 1040-4651.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199211
ENTRY DATE: Entered STN: 19930122
Last Updated on STN: 19970203
Entered Medline: 19921118

AB We have used conserved and nonconserved regions of **cDNA** **clones** for phenylalanine ammonia-lyase (PAL) and chalcone synthase (CHS) isolated from a **soybean**-nodule **cDNA** library to monitor the expression of members of the two **gene** families during the early stages of the **soybean**-Bradyrhizobium japonicum symbiosis. Our results demonstrate that subsets of the PAL and CHS **gene** families are specifically induced in **soybean** roots after infection with B. japonicum. Furthermore, by analyzing a supernodulating mutant line of **soybean** that differs from the wild-type parent in the number of successful infections, we show that the induction of PAL and CHS is related to postinfection events. Nodulated roots formed by a Nod+ Fix- strain of B. japonicum, resembling a pathogenic association, display induction of another distinct set of PAL and CHS **genes**. Our results suggest that the symbiosis-specific PAL and CHS **genes** in **soybean** are not induced by stress or pathogen interaction.

L43 ANSWER 30 OF 38 MEDLINE on STN
ACCESSION NUMBER: 91370866 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1893099
TITLE: Silencer region of a chalcone synthase promoter contains multiple binding sites for a factor, SBF-1, closely related to GT-1.
AUTHOR: Lawton M A; Dean S M; Dron M; Kooter J M; Kragh K M; Harrison M J; Yu L; Tanguay L; Dixon R A; Lamb C J
CORPORATE SOURCE: Plant Biology Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037.
SOURCE: Plant molecular biology, (1991 Feb) 16 (2) 235-49.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-S77862; GENBANK-S77864; GENBANK-S77866; GENBANK-S77870; GENBANK-S77874; GENBANK-S77877; GENBANK-X16437; GENBANK-X53596; GENBANK-X57126; GENBANK-X59469
ENTRY MONTH: 199110
ENTRY DATE: Entered STN: 19911108
Last Updated on STN: 20000303
Entered Medline: 19911021

AB Bean nuclear extracts were used in gel retardation assays and DNase I footprinting experiments to identify a protein factor, designated SBF-1, that specifically interacts with regulatory sequences in the promoter of the bean defense **gene** CHS15, which encodes the flavonoid biosynthetic enzyme chalcone synthase. SBF-1 binds to three short sequences designated boxes 1, 2 and 3 in the region -326 to - 173. This cis-element, which is involved in organ-specific expression in plant development, functions as a transcriptional silencer in electroporated protoplasts derived from undifferentiated suspension-cultured **soybean** cells. The silencer element activates in trans a co-electroporated CHS15-chloramphenicol acetyl-transferase **gene** fusion, indicating that the factor acts as a repressor in these cells. SBF-1 binding in vitro is rapid, reversible and sensitive to prior heat or protease treatment. Competitive binding assays show that boxes 1, 2 and 3 interact cooperatively, but that each box can bind the factor independently, with box 3 showing the strongest binding and box 2 the weakest binding. GGTTAA(A/T)(A/T)(A/T), which forms a consensus sequence common to all three boxes, resembles the binding site for the GT-1 factor in light-responsive elements of the pea rbcS-3A **gene**, which encodes the small subunit of ribulose bisphosphate carboxylase. Binding to the CHS15 -326 to -173 element, and to boxes 1, 2 or 3 individually, is competed by the GT-1 binding sequence of rbcS-3A, but not by a functionally inactive form, and likewise the CHS sequences can compete with authentic GT-1 sites from the rbcS-3A promoter for binding.(ABSTRACT TRUNCATED AT 250 WORDS)

L43 ANSWER 31 OF 38 MEDLINE on STN
ACCESSION NUMBER: 91016949 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2216793
TITLE: The nucleotide sequence of **gene** 3 of the **soybean** chalcone synthase multigene family.
AUTHOR: Akada S; Kung S D; Dube S K
CORPORATE SOURCE: Center for Agricultural Biotechnology, University of Maryland, College Park 20742.
SOURCE: Nucleic acids research, (1990 Oct 11) 18 (19) 5899. Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X53958
ENTRY MONTH: 199011
ENTRY DATE: Entered STN: 19910117
Last Updated on STN: 19970203
Entered Medline: 19901121

L43 ANSWER 32 OF 38 MEDLINE on STN
ACCESSION NUMBER: 90287722 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2356130
TITLE: Nucleotide sequence of one member of **soybean** chalcone synthase multi-**gene** family.
AUTHOR: Akada S; Kung S D; Dube S K
CORPORATE SOURCE: Center for Agricultural Biotechnology, University of Maryland, College Park 20742.
SOURCE: Nucleic acids research, (1990 Jun 11) 18 (11) 3398. Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X52097
ENTRY MONTH: 199007
ENTRY DATE: Entered STN: 19900824

Last Updated on STN: 19970203
Entered Medline: 19900725

L43 ANSWER 33 OF 38 MEDLINE on STN
ACCESSION NUMBER: 92404723 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2136625
TITLE: cis-regulatory elements involved in ultraviolet light regulation and plant defense.
AUTHOR: Wingender R; Rohrig H; Horicke C; Schell J
CORPORATE SOURCE: Max-Planck-Institut fur Zuchtungsforschung, Koln, Federal Republic of Germany.
SOURCE: Plant cell, (1990 Oct) 2 (10) 1019-26.
Journal code: 9208688. ISSN: 1040-4651.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199210
ENTRY DATE: Entered STN: 19921106
Last Updated on STN: 19921106
Entered Medline: 19921022

AB An elicitor-regulated transient expression system was established in **soybean** protoplasts that allowed the identification of cis-regulatory elements involved in plant defense. The 5' region of an ultraviolet (UV) light-inducible and elicitor-inducible chs **gene** (chs1) of **soybean** was subjected to deletion analysis with the help of chimeric chs-nptII/gus **gene** constructs. This analysis delimited the sequences necessary for elicitor inducibility to -175 and -134 of the chs1 promoter. The same **soybean** sequences were able to direct elicitor inducibility in parsley protoplasts, suggesting a conserved function of cis-acting elements involved in plant defense. In addition, this region of the **soybean** promoter also promotes UV light inducibility in parsley protoplasts. However, in contrast to the elicitor induction, correct regulation was not observed after UV light induction when sequences downstream of -75 were replaced by a heterologous minimal promoter. This result indicates that at least two cis-acting elements are involved in UV light induction.

L43 ANSWER 34 OF 38 MEDLINE on STN
ACCESSION NUMBER: 89386653 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2780550
TITLE: A CACGTG motif of the Antirrhinum majus chalcone synthase promoter is recognized by an evolutionarily conserved nuclear protein.
AUTHOR: Staiger D; Kaulen H; Schell J
CORPORATE SOURCE: Max-Planck-Institut fur Zuchtungsforschung, Cologne, Federal Republic of Germany.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1989 Sep) 86 (18) 6930-4.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198910
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19891024

AB In the chalcone synthase **gene** of Antirrhinum majus (snapdragon), 150 base pairs of the 5' flanking region contain cis-acting signals for UV light-induced expression. A nuclear factor, designated CG-1, specifically recognizes a hexameric motif with internal dyad symmetry, CACGTG, located within this light-responsive sequence. Binding of CG-1 is influenced by C-methylation of the CpG dinucleotide in the recognition sequence. CG-1 is a factor found in a variety of dicotyledonous plant species including Nicotiana tabacum, A. majus, Petunia hybrida, Arabidopsis thaliana, and **Glycine max**. CACGTG motifs contained within trans-acting factor recognition sites in various other plant promoters can interact with CG-1. In addition, the binding site of the human adenovirus major late transcription factor USF can compete for CG-1 binding to the chalcone synthase promoter. This suggests an evolutionary conservation of

trans-acting factor recognition sites involved in divergent mechanisms of **gene** control.

L43 ANSWER 35 OF 38 MEDLINE on STN
ACCESSION NUMBER: 89384458 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2476656
TITLE: Differential regulation of **soybean** chalcone synthase **genes** in plant defence, symbiosis and upon environmental stimuli.
AUTHOR: Wingender R; Rohrig H; Horicke C; Wing D; Schell J
CORPORATE SOURCE: Max-Planck-Institut fur Zuchtungsforschung, Koln, Federal Republic of Germany.
SOURCE: Molecular & general genetics : MGG, (1989 Aug) 218 (2) 315-22.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198910
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19970203
Entered Medline: 19891016

AB Four independent recombinant lambda **clones** hybridizing to parsley chalcone synthase (CHS) **cDNA** were isolated from a **soybean** (**Glycine max**) genomic library. Restriction fragment length polymorphism (RFLP) analysis indicated that the CHS **gene** family comprises six members. The CHS **genes** were found to be clustered with three **genes** on a 10 kb segment and pairs on others. **DNA** sequences of the 5'-, the coding-, and the 3' untranslated regions were determined for three different **genes**. A consensus alignment of the 5' regions revealed extensive homology between them for up to 150 bp upstream of the TATA box. Developmental regulation of CHS was observed in uninfected and in rhizobium-infected roots. Regulation at the level of transcription by different stimuli was investigated in the root, stem and cotyledons of **soybean** seedlings. Our results suggest a co-operative induction of CHS **genes** by wounding and elicitor treatment of cotyledons. The most rapid transcript accumulation, however, was observed in roots and stems. The induction of CHS **genes** by light was found to be UV dependent. A possible involvement of different members of the CHS **gene** family in response to elicitor versus UV treatment was analysed by the use of **gene** specific probes, and unexpectedly revealed that only CHS 1 transcription was induced by either elicitor or UV treatment of seedlings.

L43 ANSWER 36 OF 38 MEDLINE on STN
ACCESSION NUMBER: 89286138 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2500065
TITLE: Phytoalexin synthesis in **soybean** cells: elicitor induction of reductase involved in biosynthesis of 6'-deoxychalcone.
AUTHOR: Welle R; Grisebach H
CORPORATE SOURCE: Lehrstuhl fur Biochemie der Pflanzen, Biologisches Institut II der Universitat, Freiburg, Federal Republic of Germany.
SOURCE: Archives of biochemistry and biophysics, (1989 Jul) 272 (1) 97-102.
Journal code: 0372430. ISSN: 0003-9861.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198907
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19890721

AB Chromatofocusing on Mono P proved to be an efficient purification procedure for the NADPH-dependent reductase from **soybean** (**Glycine max** L.) cell cultures which acts together with chalcone synthase in the biosynthesis of 2',4',4-trihydroxychalcone (6'-deoxychalcone). By isoelectric focusing the pI of reductase was

determined to be 6.3. Addition of pure **soybean** reductase to cell-free extracts from stimulated cell cultures of parsley and bean (Phaseolus vulgaris) and from young flowers of Dahlia variabilis caused in each case synthesis of 6'-deoxychalcone. When 4-coumaroyl-CoA was replaced by caffeoyl-CoA in the reductase assay, formation of 2',4',3,4-tetrahydrochalcone (butein) was observed. A polyclonal antireductase antiserum was raised in rabbits and proved to be specific in Ouchterlony diffusion experiments, Western blots and immunotitration. The reductase antiserum showed no cross-reactivity with **soybean** chalcone synthase (CHS). A biotin/[125I]streptavidin system provided a quantitative Western blot for the reductase. Changes in the activities, amounts of protein, and **mRNA** activities of reductase and CHS were determined after challenge of **soybean** cell cultures by elicitor (from Phytophthora megasperma f.sp. glycinea or yeast). For both enzymes a pronounced and parallel increase in activity and amounts of protein was observed after elicitor addition with a maximum at about 16 h after challenge. Parallel increases in **mRNA** activities occurred earlier. The results indicate a parallel induction of de novo synthesis of reductase and CHS which coact in synthesis of 6'-deoxychalcone.

L43 ANSWER 37 OF 38 MEDLINE on STN
ACCESSION NUMBER: 86102139 MEDLINE
DOCUMENT NUMBER: PubMed ID: 3855251
TITLE: Elicitor-induced phytoalexin synthesis in **soybean** cells: changes in the activity of chalcone synthase **mRNA** and the total population of translatable **mRNA**.
AUTHOR: Grab D; Loyal R; Ebel J
SOURCE: Archives of biochemistry and biophysics, (1985 Dec) 243 (2) 523-9.
Journal code: 0372430. ISSN: 0003-9861.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 198601
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19900321
Entered Medline: 19860130

AB Rapid changes in the **mRNA** activity encoding chalcone synthase, a central enzyme involved in isoflavonoid phytoalexin synthesis, were induced in cultured cells of **soybean** (**Glycine max**) after treatment with a glucan elicitor from the cell walls of the fungus, Phytophthora megasperma f. sp. glycinea, a **soybean** pathogen. Two-dimensional gel electrophoresis of the in vitro- and in vivo-synthesized chalcone synthase showed that it consisted of a group of proteins of similar molecular weights of about 41,000, but with differing isoelectric points between pH 6.1 and pH 7.1. Total activity of chalcone synthase **mRNA** increased as early as 40 to 60 min after the onset of elicitor induction, and reached a peak at about 4 h. Treatment with the fungal elicitor caused major changes in the population of total translatable RNA as indicated by two-dimensional electrophoresis of the translation products. The **mRNA** activities for at least 16 proteins were increased and for at least 4 proteins were decreased. The elicitor-induced changes in the population of translatable **mRNA** occurred at a rate similar to that observed for chalcone synthase **mRNA** activity. Our results suggest that **soybean** cells respond to the glucan elicitor by major metabolic changes at the RNA level including the enhanced capacity for phytoalexin synthesis.

L43 ANSWER 38 OF 38 MEDLINE on STN
ACCESSION NUMBER: 84255726 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6540068
TITLE: Phytoalexin synthesis in **soybean** cells: elicitor induction of phenylalanine ammonia-lyase and chalcone synthase **mRNAs** and correlation with phytoalexin accumulation.
AUTHOR: Ebel J; Schmidt W E; Loyal R
SOURCE: Archives of biochemistry and biophysics, (1984 Jul) 232 (1) 240-8.
Journal code: 0372430. ISSN: 0003-9861.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198408
ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 19970203
Entered Medline: 19840816

AB A glucan elicitor from cell walls of the fungus Phytophthora megasperma f. sp. glycinea, a pathogen of **soybean** (**Glycine max**), induced large and rapid increases in the activities of enzymes of general phenylpropanoid metabolism, phenylalanine ammonia-lyase, and of the flavonoid pathway, acetyl-CoA carboxylase and chalcone synthase, in suspension-cultured **soybean** cells. The changes in phenylalanine ammonia-lyase and chalcone synthase activities were correlated with corresponding changes in the **mRNA** activities encoding these enzymes, as determined by enzyme synthesis in vitro in a **mRNA**-dependent reticulocyte lysate. The time courses of the elicitor-induced changes in **mRNA** activities for both enzymes were very similar with respect to each other. Following the onset of induction, the two **mRNA** activities increased significantly at 3 h, reached highest levels at 5 to 7 h, and subsequently returned to low values at 10 h. Similar degrees of induction of **mRNA** activities and of the catalytic activities of phenylalanine ammonia-lyase and chalcone synthase were observed in response to three diverse microbial compounds, the glucan elicitor from P. megasperma, xanthan, an extracellular polysaccharide from Xanthomonas campestris, and endopolygalacturonase from Aspergillus niger. However, whereas the glucan elicitor induced the accumulation of large amounts of the phytoalexin, glyceollin, in **soybean** cells, endopolygalacturonase induced only low, albeit significant, amounts; xanthan did not enhance glyceollin accumulation under the conditions of this study. This result might imply that enzymes other than phenylalanine ammonia-lyase or chalcone synthase exert an important regulatory function in phytoalexin synthesis in **soybean** cells.

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=> file reg
=> s chalcone synthase/cn
L44           1 CHALCONE SYNTHASE/CN

=> d

L44  ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   56803-04-4  REGISTRY
CN   Synthase, flavanone (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Anthocyanidin synthase
CN   Chalcone synthase
CN   Chalcone synthetase
CN   E.C. 2.3.1.74
CN   Flavanone synthase
CN   Flavanone synthetase
CN   Naringenin-chalcone synthase
MF   Unspecified
CI   MAN
LC   STN Files:   AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS,
       CASREACT, CIN, EMBASE, NAPRALERT, PROMT, TOXCENTER, USPAT2, USPATFULL
DT.CA  CAplus document type:  Conference; Dissertation; Journal; Patent
RL.P   Roles from patents:  ANST (Analytical study); BIOL (Biological study);
       MSC (Miscellaneous); OCCU (Occurrence); PREP (Preparation); PROC
       (Process); PRP (Properties); USES (Uses)
RLD.P  Roles for non-specific derivatives from patents:  BIOL (Biological
       study); PREP (Preparation); PRP (Properties)
RL.NP  Roles from non-patents:  ANST (Analytical study); BIOL (Biological
       study); FORM (Formation, nonpreparative); MSC (Miscellaneous); OCCU
       (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); USES
       (Uses); NORL (No role in record)
RLD.NP Roles for non-specific derivatives from non-patents:  BIOL (Biological
       study); OCCU (Occurrence); PROC (Process); PRP (Properties)
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851 REFERENCES IN FILE CA (1907 TO DATE)
4 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
852 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> s chalcone/cn
L45 1 CHALCONE/CN

=> d

L45 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN
RN 94-41-7 REGISTRY
CN 2-Propen-1-one, 1,3-diphenyl- (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN **Chalcone (8CI)**
OTHER NAMES:
CN .alpha.-Benzylideneacetophenone
CN .beta.-Benzoylstyrene
CN .beta.-Phenylacrylophenone
CN .omega.-Benzylideneacetophenone
CN 1,3-Diphenyl-1-propen-3-one
CN 1,3-Diphenyl-2-propen-1-one
CN 1,3-Diphenyl-2-propenone
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CN 1-Benzoyl-1-phenylethene
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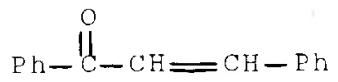
(*File contains numerically searchable property data)
Other Sources: EINECS**, NDSL**, TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)
DT.CA CAplus document type: Book; Conference; Dissertation; Journal; Patent; Preprint; Report
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); MSC (Miscellaneous); OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); RACT (Reactant or reagent); USES (Uses); NORL (No role in record)
RLD.P Roles for non-specific derivatives from patents: ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); RACT (Reactant or reagent); USES (Uses)
RL.NP Roles from non-patents: ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); MSC (Miscellaneous); OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); RACT (Reactant or reagent); USES (Uses); NORL (No role in record)

RLD.NP Roles for non-specific derivatives from non-patents: ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); MSC (Miscellaneous); OCCU (Occurrence); PREP (Preparation); PROC (Process); PRP (Properties); RACT (Reactant or reagent); USES (Uses)



PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

3580 REFERENCES IN FILE CA (1907 TO DATE)
258 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
3587 REFERENCES IN FILE CAPLUS (1907 TO DATE)
14 REFERENCES IN FILE CAOLD (PRIOR TO 1967)

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